



SEQUENCE LISTING

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<120> DIMERIZING PEPTIDES

<130> 8325-1004 / M4-US1

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<160> 83

<170> PatentIn Ver. 2.0

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<223> Description of Artificial Sequence: exemplary motif characterizing C2H2 class proteins

(B)
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<221> SITE

<222> (2)...(5)

<223> where Xaa is any amino acid

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<222> (4)...(5)

<223> where Xaa may be present or absent

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<223> where Xaa may be present or absent

<400> 1

Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa His Xaa Xaa Xaa Xaa Xaa His

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<210> 2
<211> 4
<212> PRT
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<223> Description of Artificial Sequence: D-able
subsite

<400> 2
Asn Asn Gly Lys
1

<210> 3
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<220>
<223> Description of Artificial Sequence: zinc finger
protein bind sequence

<400> 3
ggcgttagac

9

<210> 4
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<220>
<223> Description of Artificial Sequence: zinc finger
protein bind sequence

<400> 4
ggcgacgta

9

<210> 5
<211> 5
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<220>
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linker

<400> 5
Thr Gly Glu Lys Pro
1 5

<210> 6
<211> 5
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<213> Artificial Sequence

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<400> 6
Gly Gly Gly Gly Ser
1 5

<210> 7
<211> 8
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<223> Description of Artificial Sequence: linker

<400> 7
Gly Gly Arg Arg Gly Gly Gly Ser
1 5

<210> 8
<211> 9
<212> PRT
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<223> Description of Artificial Sequence: linker

<400> 8
Leu Arg Gln Arg Asp Gly Glu Arg Pro
1 5

<210> 9
<211> 12
<212> PRT
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<223> Description of Artificial Sequence: linker

<400> 9
Leu Arg Gln Lys Asp Gly Gly Ser Glu Arg Pro
1 5 10

<210> 10
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<400> 10

Leu Arg Gln Lys Asp Gly Gly Ser Gly Gly Ser Glu Arg Pro
1 5 10 15

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finger of zinc finger protein

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<223> where Xaa may be present or absent

<400> 11
Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa His Xaa Xaa Xaa Xaa His
20 25

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domain F1

<400> 12
Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp
1 5 10 15

Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys Pro
20 25 30

<210> 13
<211> 28
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domain F2

<400> 13
Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu
1 5 10 15

Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro
20 25

<210> 14
<211> 38
<212> DNA
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<220>
<223> Description of Artificial Sequence: DNA binding
site

<400> 14
ggttgcagtg ggcgcgcccc cagtaacttga acgttaacg 38

<210> 15
<211> 34
<212> DNA
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site

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cgttacgttc aagtactgtg ggcgcgcccc ctgc 34

<210> 16
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site

<400> 16
tgggcgtatg ct 12

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<211> 12
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<400> 17
agcatacgcc ca 12

<210> 18
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gaaattcctg atcaagatct ggtcacgtcc ataggctagg catgtcaagg ctgttatg 57

<210> 19
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gggatccact cgcgaacgca tcctttagt gggcgcccc acatacagcc ttgacat 57

<210> 20
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<400> 20
tgggcgcgcc ca 12

<210> 21
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<400> 21
atgggcgcgc ccat 14

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<223> "Arg" is numbered 103

<400> 22
His Pro Met Asn Asn Leu Leu Asn Tyr Val Val Pro Lys Met Arg
1 5 10 15

<210> 23
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<223> Description of Artificial Sequence: DNA site used for affinity selection

<400> 23
gcagtggcg cgcccacagt acttgaacgt aacg 34

<210> 24
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<220>
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<400> 24
Gly Gly Gly Gln Trp Leu Gly Thr Trp Glu Trp Tyr Gly Pro Lys
1 5 10 15

<210> 25
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 25

Tyr Glu Lys Ile Ser Val Glu Gly Ile Lys Asp Val Arg Val Arg
1 5 10 15

<210> 26
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 26
Asn Val Ser Ile Glu Gly Val Leu Lys Tyr Tyr Arg Gly Leu Arg
1 5 10 15

<210> 27
<211> 15
<212> PRT
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<220>
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<400> 27
Arg Ser Cys Gly Leu Asp Tyr Glu Gly Tyr Trp Leu Lys Leu Lys
1 5 10 15

<210> 28
<211> 15
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<220>
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<400> 28
Ser Arg Trp Leu Glu Glu Val Ser Arg Leu Leu Leu Leu Arg
1 5 10 15

<210> 29
<211> 15
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<400> 29
Gly Glu Ala Leu Asp Arg Phe Glu Arg Glu Met Lys Leu Met Arg
1 5 10 15

<210> 30
<211> 5

<212> PRT
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block reoptimization sequence

<400> 30
Gly Gly Gly Gln Trp
1 5

<210> 31
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block reoptimization sequence

<400> 31
His Pro Met Asn Asn
1 5

<210> 32
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<400> 32
Pro Pro Ser Thr Glu
1 5

<210> 33
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Gln Lys Tyr Gly Asp
1 5

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Glu Asn Tyr Glu Lys
1 5

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<400> 35
Leu Gly Thr Trp Glu
1 5

<210> 36
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<400> 36
Leu Leu Asn Tyr Lys
1 5

<210> 37
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<400> 37
Leu Leu Asn Tyr Val
1 5

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<400> 38
Leu Leu Asp Tyr Ile
1 5

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Leu Leu Asn Tyr Ile
1 5

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Leu Leu Gln Tyr Val
1 5

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Leu Leu Glu Tyr Lys
1 5

<210> 42
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<400> 42
Leu Leu Asp Tyr Val
1 5

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Leu Leu Asn Tyr Val
1 5

<210> 44
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Trp Tyr Gly Pro Lys
1 5

<210> 45
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His Pro Lys Met Lys
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<210> 46
<211> 5
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block reoptimization sequence

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Pro Ala Lys Ile Arg

<210> 47
<211> 5
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block reoptimization sequence

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Val Pro Lys Ser Arg
1 5

<210> 48
<211> 5
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Val Pro Arg Leu Lys
1 5

<210> 49
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Ala Pro Lys Leu Arg
1 5

<210> 50
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His Ala Lys Ile Arg
1 5

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Val Val Lys Met Arg
1 5

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Pro Val Lys Met Arg
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Val Pro Lys Gln Arg
1 5

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Val Pro Lys Met Arg
1 5

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Val Arg Lys Leu Arg
1 5

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Ser Arg Trp Leu Glu
1 5

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Phe Arg Trp Leu Glu
1 5

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Gln Pro Trp Leu Thr
1 5

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Pro Pro Trp Leu Ile
1 5

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<400> 60
Pro Pro Trp Leu Lys
1 5

<210> 61
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<400> 61
Pro Ala Trp Leu Thr
1 5

<210> 62
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Pro Ala Trp Leu Ala
1 5

<210> 63
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<400> 63
Trp Ala Trp Leu Asp
1 5

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Pro Thr Trp Leu Thr
1 5

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<400> 65
Glu Glu Val Ser Arg
1 5

<210> 66
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block reoptimization sequence

<400> 66
Glu Tyr Leu Glu Ser
1 5

<210> 67
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block reoptimization sequence

<400> 67
Asp Tyr Val Thr Gln
1 5

<210> 68
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block reoptimization sequence

<400> 68
Asp Tyr Leu Ala Asp
1 5

<210> 69
<211> 5
<212> PRT
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block reoptimization sequence

<400> 69
Glu Tyr Leu Thr Phe
1 5

<210> 70
<211> 5
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block reoptimization sequence

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Gln Tyr Leu Glu Asp
1 5

<210> 71
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block reoptimization sequence

<400> 71
Asp Tyr Val Ser Gln

<210> 72
<211> 5
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block reoptimization sequence

<400> 72
Ser Tyr Leu Asp Lys
1 5

<210> 73
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<220>
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block reoptimization sequence

<400> 73
Glu Tyr Met Ser Asp
1 5

<210> 74
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<400> 74
Leu Leu Leu Leu Arg
1 5

<210> 75
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block reoptimization sequence

<400> 75
Met Arg Leu Trp Arg
1 5

<210> 76
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<400> 76
Met Arg Gly Trp Lys
1 5

<210> 77
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<400> 77
Met Arg Lys Trp Arg
1 5

<210> 78
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block reoptimization sequence

<400> 78
Met Arg Lys Trp Lys
1 5

<210> 79
<211> 5
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<220>
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block reoptimization sequence

<400> 79
Met Gly Val Met Arg
1 5

<210> 80
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<220>
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<400> 80
Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser
1 5 10 15

Asp Glu Leu Thr Arg His Ile Arg Ile His Thr
20 25

<210> 81
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GLI1

<400> 81
Glu Thr Asp Cys Arg Trp Asp Gly Cys Ser Gln Glu Phe Asp Ser Gln
1 5 10 15

Glu Gln Leu Val His His Ile Asn Ser Glu His Ile
20 25

<210> 82
<211> 30
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GLI2

<400> 82
Glu Phe Val Cys His Trp Gly Gly Cys Ser Arg Glu Leu Arg Pro Phe
1 5 10 15

Lys Ala Gln Tyr Met Leu Val Val His Met Arg Arg His Thr
20 25 30

<210> 83
<211> 27
<212> PRT
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<220>
<223> Description of Artificial Sequence: SWI5

<400> 83
Thr Phe Glu Cys Leu Phe Pro Gly Cys Thr Lys Thr Phe Lys Arg Arg
1 5 10 15

Tyr Asn Ile Arg Ser His Ile Gln Thr His Leu
20 25

*B1
None*
